

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/990,046A
Source: 1FW16
Date Processed by STIC: 3/28/05

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 03/28/2005

PATENT APPLICATION: US/09/990,046A

TIME: 09:11:50

Input Set : A:\P1405R1C1.txt

Output Set: N:\CRF4\03282005\I990046A.raw

3 <110> APPLICANT: de Sauvage, Frederic
 4 Carpenter, David A.
 6 <120> TITLE OF INVENTION: Patched-2 Antibodies
 8 <130> FILE REFERENCE: P1405R1C1
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/990,046A
 C--> 11 <141> CURRENT FILING DATE: 2001-11-20
 13 <150> PRIOR APPLICATION NUMBER: US 60/081,884
 14 <151> PRIOR FILING DATE: 1998-04-15
 16 <160> NUMBER OF SEQ ID NOS: 24
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 4030
 20 <212> TYPE: DNA
 21 <213> ORGANISM: Homo sapiens
 23 <400> SEQUENCE: 1
 24 gttatttcag gccatggtgt tgcgccgaat taattcccga tccagacatg 50
 26 ataagataca ttgatgagtt tggacaaacc acaactagaa tgcagtgaag 100
 28 aaaatgcttt atttgtgaaa tttgtgatgc tattgcttta tttgtaacca 150
 30 ttataagctg caataaaca gttgggccat ggcggccaag cttctgcagg 200
 32 tcgactctag aggatccccg ggggaattccg gcatgactcg atcgccgcc 250
 34 ctccagagagc tgcccccgag ttacacaccc ccagctcgaa ccgcagcacc 300
 36 ccagatccta gctgggagcc tgaaggctcc actctggctt cgtgcttact 350
 38 tccagggcct gctcttctct ctgggatgag ggatccagag acattgtggc 400
 40 aaagtgtctt ttctgggact gttggccttt ggggcccctg cattaggtct 450
 42 ccgcatggcc attattgaga caaacttggg acagctctgg gtagaagtgg 500
 44 gcagccgggt gagccaggag ctgcattaca ccaaggagaa gctgggggag 550
 46 gaggctgcat acacctctca gatgctgata cagaccgcac gccaggaggg 600
 48 agagaacatc ctccaccccg aagcacttgg cctccacctc caggcagccc 650
 50 tcatgcccag taaagtccaa gtatcactct atgggaagtc ctgggatttg 700
 52 aacaaaatct gctacaagtc aggagttccc cttattgaaa atggaatgat 750
 54 tgagtggatg attgagaagc tgtttccgtg cgtgatcctc acccccctcg 800
 56 actgcttctg ggaggggagcc aaactccaag ggggctccgc ctacctgccc 850
 58 ggccgcccgg atatccagtg gaccaacctg gatccagagc agctgctgga 900
 60 ggagctgggt ccctttgcct cccttgaggg cttccgggag ctgctagaca 950
 62 aggcacaggt gggccaggcc tacgtggggc ggccctgtct gcaccctgat 1000
 64 gacctccact gccacactag tgcccccaac catcacagca ggcaggctcc 1050
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 68 tcatgcactg gcaggaggaa ttgctgctgg gaggcatggc cagagacccc 1150
 70 caaggagagc tgctgagggc agaggccctg cagagcacct tcttgctgat 1200
 72 gagtccccgc cagctgtacg agcatttccg gggtgactat cagacacatg 1250
 74 acattggctg gagtggagg caggccagca cagtgtctaca agcctggcag 1300
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 78 gcagatccat gccttctcct ccaccacct ggatgacatc ctgcatgctg 1400
 80 tctctgaagt cagtgtgtgc cgtgtgggtg gaggctatct gctcatgctg 1450

p.6

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82 gcctatgcct gtgtgaccat gctgcggttg gactgcgccc agtcccaggg 1500
84 ttccgtgggc cttgccgggg tactgctggt ggccctggcg gtggcctcag 1550
86 gccttgggct ctgtgccctg ctgcgcatca ccttcaatgc tgccactacc 1600
88 caggtgctgc ctttcttggt tctgggaatc ggcgtggatg acgtattcct 1650
90 gctggcgcat gccttcacag aggctctgcc tggcaccctt ctccaggagc 1700
92 gcatgggcga gtgtctgcag cgcacgggca ccagtgtcgt actcacatcc 1750
94 atcaacaaca tggccgcctt cctcatggct gccctcgttc ccatccctgc 1800
96 gctgcgagcc ttctccctac aggcggccat agtggttggc tgcaccttg 1850
98 tagccgtgat gcttgtcttc ccagccatcc tcagcctgga cctacggcgg 1900
100 cgccactgcc agcgccttga tgtgctctgc tgcttctcca gtccctgctc 1950
102 tgctcagggtg attcagatcc tgccccagga gctgggggac gggacagtac 2000
104 cagtgggcat tgcccacctc actgccacag ttcaagcctt taccactgt 2050
106 gaagccagca gccagcatgt ggtcaccatc ctgcctcccc aagcccacct 2100
108 ggtgccccca cctcttgacc cactgggctc tgagctcttc agccctggag 2150
110 ggtccacacg ggaccttcta ggccaggagg aggagacaag gcagaaggca 2200
112 gcctgcaagt ccctgccctg tgcccgctgg aatcttgccc atttcgccc 2250
114 ctatcagttt gccccgttgc tgctccagtc acatgccaag gccatcgtgc 2300
116 tgggtgctctt tgggtgctctt ctgggcctga gcctctacgg agccaccttg 2350
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122 ccctggtgac ccagggtggc ttgactacg cccattccca acgcgcctc 2500
124 tttgatctgc accagcgctt cagttccctc aaggcgggtg tgccccacc 2550
126 ggccacccag gcaccccgca cctggctgca ctattaccgc aactgggtac 2600
128 agggaatcca ggetgccttt gaccaggact gggcttctgg gcgcatcacc 2650
130 cgccactcgt accgcaatgg ctctgaggat ggggcccctg cctacaagct 2700
132 gctcatccag actggagacg cccaggagcc tctggatttc agccagctga 2750
134 ccacaaggaa gctggtggac agagagggac tgattccacc cgagctcttc 2800
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138 ctacacggcc aacttctacc ccccacctc tgaatggctg cagacaaat 2900
140 acgacaggcc gggggagaac ctctgcaccc cgccagctca gcccttggag 2950
142 tttgcccagt tccccttccct gctgcgtggc ctccagaaga ctgcagactt 3000
144 tgtggaggcc atcgaggggg cccgggcagc atgcgcagag gccggccagg 3050
146 ctggggtgca cgcctacccc agcggctccc ccttctctt ctgggaacag 3100
148 tatctgggcc tgcggcgtg ctctctgctg gccgtctgca tctgtgtgt 3150
150 gtgcactttc ctgctctgtg ctctgctgct cctcaacccc tggacggctg 3200
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162 gctcatgctt gctggttccc actttgactt cattgtaagg tacttctttg 3500
164 cggcgtgac agtgetcacg ctctgggccc tctccatgg actcgtgctg 3550
166 ctgctgtgc tgetgtccat cctgggccc cgccagagg tgatacagat 3600
168 gtacaaggaa agcccagaga tctgagtc accagctcca cagggaggcg 3650
170 ggcttaggtg gggggcatcc tctccctgc cccagagctt tgccagagtg 3700
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174 catccatcca gcccctgatg agcccccttg gtcccctgct gccactagct 3800
176 ctggcaacct cagttccagg ggaccaggtc cagccactgg gtgaaagagc 3850
178 agctgaagca cagagacct gtgtggggcg tgtggggtca ctgggaagca 3900

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180 ctgggtctgg tgtagacgc aggacggacc cctggagggc cctgctgctg 3950
182 ctgcatcccc tctcccgacc cagctgtcat gggcctccct gatatcgaat 4000
184 tcaatcgata gaaccgaggt gcagttggac 4030
186 <210> SEQ ID NO: 2
187 <211> LENGTH: 1203
188 <212> TYPE: PRT
189 <213> ORGANISM: Homo sapiens
191 <400> SEQUENCE: 2
192 Met Thr Arg Ser Pro Pro Leu Arg Glu Leu Pro Pro Ser Tyr Thr
193 1 5 10 15
195 Pro Pro Ala Arg Thr Ala Ala Pro Gln Ile Leu Ala Gly Ser Leu
196 20 25 30
198 Lys Ala Pro Leu Trp Leu Arg Ala Tyr Phe Gln Gly Leu Leu Phe
199 35 40 45
201 Ser Leu Gly Cys Gly Ile Gln Arg His Cys Gly Lys Val Leu Phe
202 50 55 60
204 Leu Gly Leu Leu Ala Phe Gly Ala Leu Ala Leu Gly Leu Arg Met
205 65 70 75
207 Ala Ile Ile Glu Thr Asn Leu Glu Gln Leu Trp Val Glu Val Gly
208 80 85 90
210 Ser Arg Val Ser Gln Glu Leu His Tyr Thr Lys Glu Lys Leu Gly
211 95 100 105
213 Glu Glu Ala Ala Tyr Thr Ser Gln Met Leu Ile Gln Thr Ala Arg
214 110 115 120
216 Gln Glu Gly Glu Asn Ile Leu Thr Pro Glu Ala Leu Gly Leu His
217 125 130 135
219 Leu Gln Ala Ala Leu Thr Ala Ser Lys Val Gln Val Ser Leu Tyr
220 140 145 150
222 Gly Lys Ser Trp Asp Leu Asn Lys Ile Cys Tyr Lys Ser Gly Val
223 155 160 165
225 Pro Leu Ile Glu Asn Gly Met Ile Glu Trp Met Ile Glu Lys Leu
226 170 175 180
228 Phe Pro Cys Val Ile Leu Thr Pro Leu Asp Cys Phe Trp Glu Gly
229 185 190 195
231 Ala Lys Leu Gln Gly Gly Ser Ala Tyr Leu Pro Gly Arg Pro Asp
232 200 205 210
234 Ile Gln Trp Thr Asn Leu Asp Pro Glu Gln Leu Leu Glu Glu Leu
235 215 220 225
237 Gly Pro Phe Ala Ser Leu Glu Gly Phe Arg Glu Leu Leu Asp Lys
238 230 235 240
240 Ala Gln Val Gly Gln Ala Tyr Val Gly Arg Pro Cys Leu His Pro
241 245 250 255
243 Asp Asp Leu His Cys Pro Pro Ser Ala Pro Asn His His Ser Arg
244 260 265 270
246 Gln Ala Pro Asn Val Ala His Glu Leu Ser Gly Gly Cys His Gly
247 275 280 285
249 Phe Ser His Lys Phe Met His Trp Gln Glu Glu Leu Leu Leu Gly
250 290 295 300
252 Gly Met Ala Arg Asp Pro Gln Gly Glu Leu Leu Arg Ala Glu Ala

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253		305		310		315
255	Leu Gln Ser Thr	Phe Leu Leu Met Ser	Pro Arg Gln Leu Tyr	Glu		
256		320		325		330
258	His Phe Arg Gly	Asp Tyr Gln Thr His	Asp Ile Gly Trp Ser	Glu		
259		335		340		345
261	Glu Gln Ala Ser	Thr Val Leu Gln Ala	Trp Gln Arg Arg Phe	Val		
262		350		355		360
264	Gln Leu Ala Gln	Glu Ala Leu Pro Glu	Asn Ala Ser Gln Gln	Ile		
265		365		370		375
267	His Ala Phe Ser	Ser Thr Thr Leu Asp	Asp Ile Leu His Ala	Phe		
268		380		385		390
270	Ser Glu Val Ser	Ala Ala Arg Val Val	Gly Gly Tyr Leu Leu	Met		
271		395		400		405
273	Leu Ala Tyr Ala	Cys Val Thr Met Leu	Arg Trp Asp Cys Ala	Gln		
274		410		415		420
276	Ser Gln Gly Ser	Val Gly Leu Ala Gly	Val Leu Leu Val Ala	Leu		
277		425		430		435
279	Ala Val Ala Ser	Gly Leu Gly Leu Cys	Ala Leu Leu Gly Ile	Thr		
280		440		445		450
282	Phe Asn Ala Ala	Thr Thr Gln Val Leu	Pro Phe Leu Ala Leu	Gly		
283		455		460		465
285	Ile Gly Val Asp	Asp Val Phe Leu Leu	Ala His Ala Phe Thr	Glu		
286		470		475		480
288	Ala Leu Pro Gly	Thr Pro Leu Gln Glu	Arg Met Gly Glu Cys	Leu		
289		485		490		495
291	Gln Arg Thr Gly	Thr Ser Val Val Leu	Thr Ser Ile Asn Asn	Met		
292		500		505		510
294	Ala Ala Phe Leu	Met Ala Ala Leu Val	Pro Ile Pro Ala Leu	Arg		
295		515		520		525
297	Ala Phe Ser Leu	Gln Ala Ala Ile Val	Val Gly Cys Thr Phe	Val		
298		530		535		540
300	Ala Val Met Leu	Val Phe Pro Ala Ile	Leu Ser Leu Asp Leu	Arg		
301		545		550		555
303	Arg Arg His Cys	Gln Arg Leu Asp Val	Leu Cys Cys Phe Ser	Ser		
304		560		565		570
306	Pro Cys Ser Ala	Gln Val Ile Gln Ile	Leu Pro Gln Glu Leu	Gly		
307		575		580		585
309	Asp Gly Thr Val	Pro Val Gly Ile Ala	His Leu Thr Ala Thr	Val		
310		590		595		600
312	Gln Ala Phe Thr	His Cys Glu Ala Ser	Ser Gln His Val Val	Thr		
313		605		610		615
315	Ile Leu Pro Pro	Gln Ala His Leu Val	Pro Pro Pro Ser Asp	Pro		
316		620		625		630
318	Leu Gly Ser Glu	Leu Phe Ser Pro Gly	Gly Ser Thr Arg Asp	Leu		
319		635		640		645
321	Leu Gly Gln Glu	Glu Glu Thr Arg Gln	Lys Ala Ala Cys Lys	Ser		
322		650		655		660
324	Leu Pro Cys Ala	Arg Trp Asn Leu Ala	His Phe Ala Arg Tyr	Gln		
325		665		670		675

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327	Phe	Ala	Pro	Leu	Leu	Leu	Gln	Ser	His	Ala	Lys	Ala	Ile	Val	Leu
328					680					685					690
330	Val	Leu	Phe	Gly	Ala	Leu	Leu	Gly	Leu	Ser	Leu	Tyr	Gly	Ala	Thr
331					695					700					705
333	Leu	Val	Gln	Asp	Gly	Leu	Ala	Leu	Thr	Asp	Val	Val	Pro	Arg	Gly
334					710					715					720
336	Thr	Lys	Glu	His	Ala	Phe	Leu	Ser	Ala	Gln	Leu	Arg	Tyr	Phe	Ser
337					725					730					735
339	Leu	Tyr	Glu	Val	Ala	Leu	Val	Thr	Gln	Gly	Gly	Phe	Asp	Tyr	Ala
340					740					745					750
342	His	Ser	Gln	Arg	Ala	Leu	Phe	Asp	Leu	His	Gln	Arg	Phe	Ser	Ser
343					755					760					765
345	Leu	Lys	Ala	Val	Leu	Pro	Pro	Pro	Ala	Thr	Gln	Ala	Pro	Arg	Thr
346					770					775					780
348	Trp	Leu	His	Tyr	Tyr	Arg	Asn	Trp	Leu	Gln	Gly	Ile	Gln	Ala	Ala
349					785					790					795
351	Phe	Asp	Gln	Asp	Trp	Ala	Ser	Gly	Arg	Ile	Thr	Arg	His	Ser	Tyr
352					800					805					810
354	Arg	Asn	Gly	Ser	Glu	Asp	Gly	Ala	Leu	Ala	Tyr	Lys	Leu	Leu	Ile
355					815					820					825
357	Gln	Thr	Gly	Asp	Ala	Gln	Glu	Pro	Leu	Asp	Phe	Ser	Gln	Leu	Thr
358					830					835					840
360	Thr	Arg	Lys	Leu	Val	Asp	Arg	Glu	Gly	Leu	Ile	Pro	Pro	Glu	Leu
361					845					850					855
363	Phe	Tyr	Met	Gly	Leu	Thr	Val	Trp	Val	Ser	Ser	Asp	Pro	Leu	Gly
364					860					865					870
366	Leu	Ala	Ala	Ser	Gln	Ala	Asn	Phe	Tyr	Pro	Pro	Pro	Pro	Glu	Trp
367					875					880					885
369	Leu	His	Asp	Lys	Tyr	Asp	Thr	Thr	Gly	Glu	Asn	Leu	Arg	Ile	Pro
370					890					895					900
372	Pro	Ala	Gln	Pro	Leu	Glu	Phe	Ala	Gln	Phe	Pro	Phe	Leu	Leu	Arg
373					905					910					915
375	Gly	Leu	Gln	Lys	Thr	Ala	Asp	Phe	Val	Glu	Ala	Ile	Glu	Gly	Ala
376					920					925					930
378	Arg	Ala	Ala	Cys	Ala	Glu	Ala	Gly	Gln	Ala	Gly	Val	His	Ala	Tyr
379					935					940					945
381	Pro	Ser	Gly	Ser	Pro	Phe	Leu	Phe	Trp	Glu	Gln	Tyr	Leu	Gly	Leu
382					950					955					960
384	Arg	Arg	Cys	Phe	Leu	Leu	Ala	Val	Cys	Ile	Leu	Leu	Val	Cys	Thr
385					965					970					975
387	Phe	Leu	Val	Cys	Ala	Leu	Leu	Leu	Leu	Asn	Pro	Trp	Thr	Ala	Gly
388					980					985					990
390	Leu	Ile	Val	Leu	Val	Leu	Ala	Met	Met	Thr	Val	Glu	Leu	Phe	Gly
391					995					1000					1005
393	Ile	Met	Gly	Phe	Leu	Gly	Ile	Lys	Leu	Ser	Ala	Ile	Pro	Val	Val
394					1010					1015					1020
396	Ile	Leu	Val	Ala	Ser	Val	Gly	Ile	Gly	Val	Glu	Phe	Thr	Val	His
397					1025					1030					1035
399	Val	Ala	Leu	Gly	Phe	Leu	Thr	Thr	Gln	Gly	Ser	Arg	Asn	Leu	Arg

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 03/28/2005
PATENT APPLICATION: US/09/990,046A TIME: 09:11:51

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 20,27,135,156,210

Seq#:4; N Pos. 143

Seq#:6; N Pos. 13,14

VERIFICATION SUMMARY

DATE: 03/28/2005

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Input Set : A:\P1405R1C1.txt

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L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:446 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
M:341 Repeated in SeqNo=3
L:471 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:100
L:502 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0